



[17] RN RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).  
 RX MEDLINE: 20020155.  
 RX PUBLISHER: M A Bahtur, R M Hanson, G T Kallio, K, Remington S.J.;  
 RX Author: M A Bahtur, R M Hanson, G T Kallio, K, Remington S.J.;  
 RX Structural and spectral response of green fluorescent protein  
 RX to changes in pH \*.  
 RL Biochemistry 38:5256-5310(1999).

[1] - FUNCTION: ENERGY TRANSFER ACCEPTOR. ITS ROLE IS TO TRANSMIT THE CC BLUE CHEMILUMINESCENCE OF THE PROTEIN TRANSFER. FLUORESCES IN VIVO UPON CC RECEIVING ENERGY FROM THE CA++-ACTIVATED PHOTOPROTEIN AEQORIN.  
 CC ABSORBS LIGHT MAINLY AT 395 NM AND EXHIBITS A SMALLER EMISSION SPECTRUM CC PEAK AT 509 NM. THE FLUORESCENCE PEAK IS AT 470 NM.

[1] - SUBUNIT: MONOMER.  
 CC -1 TISSUE SPECIFICITY: PHOTOCYTES.  
 CC -1 PTM: CONTAINS A COVALENTLY ATTACHED CHROMOPHORE, WHICH IS COMPOSED CC OF MODIFIED AMINO ACID RESIDUES. THE CHROMOPHORE IS FORMED UPON CC CRYSTALLIZATION OF THE RESIDUES SER-DEHYDROTYR-GLY.

[1] - BIOTECHNOLOGY: Has become a useful and ubiquitous tool for making chimeric proteins of GFP linked to other proteins where its functions as a fluorescent Protein tag. GFP tolerates N- and C-terminal fusion to a broad variety of proteins. It has been expressed in bacteria, yeast, silicon mold, plants, drosophila, zebrafish and mammalian cells. As a non-invasive fluorescent marker it is very useful as a label for a wide range of applications such as tracking cell migration, gene expression, reporter gene expression or as a measure of protein-protein interactions.

[1] - DATABASE: NAME=Protein Spotlight; URL=<http://www.isb-sib.ch/announce/PROTEIN.html>;  
 CC NOT=Issue 11 of June 2001.  
 CC URL=<http://www.exapey.org/spotlight/article8.asp?l0101.htm>.  
 CC

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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch).

DR PMID: 16654; AAA27721; -.  
 DR ENZY: M6653; AAA27721; -.  
 DR ENZY: L29345; AAA27721; -.  
 DR PDB: 1GF; 1.JAN.97.  
 DR PDB: 1JEA; 08.AUG.96.  
 DR PDB: 1JEM; 06.JUN.97.  
 DR PDB: 1EAM; 20.AUG.97.  
 DR PDB: 1EAO; 20.AUG.97.  
 DR PDB: 1EAP; 20.AUG.97.  
 DR PDB: 1EAS; 20.AUG.97.  
 DR PDB: 1EAT; 20.AUG.97.  
 DR PDB: 1EAV; 20.AUG.97.  
 DR PDB: 1EAW; 20.AUG.97.  
 DR PDB: 1EAX; 20.AUG.97.  
 DR PDB: 1EAY; 20.AUG.97.  
 DR PDB: 1EAZ; 20.AUG.97.  
 DR PDB: 1EBC; 07.JUL.97.  
 DR PDB: 1YFP; 28.OCT.98.  
 DR Interpro: IPR00786; Green\_f1-protein.  
 DR Printn: PRO11529; GFP; 1.  
 DR Printn: PRO13175; Green\_f1-protein; 1.  
 DR Luminescence; 3D structure.  
 SITE 65 67 MODIFIED TO FORM THE CHROMOPHORE.  
 PT VARIANT 100 100 F -> Y.  
 PT VARIANT 108 108 T -> S.  
 PT VARIANT 141 141 I -> M.  
 PT VARIANT 219 219 V -> I.  
 PT CONFLICT 25 25 H -> O ((IN REF 2);  
 PT CONFLICT 157 157 Q -> P ((IN REF 2);  
 PT CONFLICT 174 174 E -> D ((IN REF 2);  
 SITE 238 AA: 26886 MW: EA5ASF21F6B605 CRC64;



San-Gupta M., Liok R., Pleig U., Wiedenthal R.K., Hegemann J.H.; The sequence of  $\lambda$ XIV, 41,283 bp element from the left arm of chromosome XIV from Saccharomyces cerevisiae is between the RII and the RII $\alpha$  genes. *J. Mol. Biol.* 212: 505-514 (1990).

TEMPERATURE SENSITIVE MUTANTS  
MEDLINE ID: 92161663 - Pubmed 137345;

Sarai H., Ropp P.A., Johnson A.L., Johnson L.H., Morrison A., Sugino H., the probable homolog of mammalian DNA Polymerase epsilon replicates chromosomal DNA in the yeast, *Saccharomyces cerevisiae*. *Nature* 311: 713-740 (1984).

-1- PROKARYOTIC DNA POLYMERASE II PARTICIPATES IN CHROMOSOMAL DNA REPLICATION: N deoxyribonucleoside triphosphate = N diphosphate  
MEDLINE ID: 92161663 - Pubmed 137345;

-1- SSBONI (N) CONSISTS OF FIVE SUBUNITS (200 kDa, 80 kDa, 34 kDa, 30 kDa, 29 kDa);  
-1- SUBCELLULAR LOCALIZATION: Nucleus;  
-1- DOMAIN IN THE DNA POLYMERASE ACTIVITY DOMAIN RESIDES IN THE N-TERMINAL PORTION OF THE PROTEIN, WHILE THE C-TERMINUS IS NECESSARY FOR CONFIRMING SUBUNITS B AND C;  
-1- MISCELLANEOUS IN EUKARYOTES THERE ARE FIVE DNA POLYMERASES;  
-1- ALPHABETICALLY GAMMA, DELTA, EPSILON WHICH ARE RESPONSIBLE FOR DIFFERENT REACTIONS ON DNA; SINEWESIS IS SIMILARITY WITH POLYMERASE B FAMILY. HIGH SIMILARITY WITH MAMMALIAN DNA POLYMERASE Epsilon;

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SLAP-BACLI STANDARD:		PRT:	874 AA.
ID	SLAP-BACLI		
SDID	BACLI		
PA9057		PRT:	
DL			
DT	01-FEB-1996 (Rel. 33. Created)		
DR	01-FEB-1996 (Rel. 33. Last sequence update)		
DR	01-FEB-1997 (Rel. 35. Last annotation update)		
DR	01-NOV-1997 (Rel. 35. Last sequence update)		
DR	S-layer protein precursor (Surface layer Protein).		
OS	Bacillus licheniformis		
OC	Bacteria; Firmicutes; Bactillales; Bactillaceae; Bacillus.		
RN	[1] NM_001020292		
RP	SEQUENCE FROM N.A.		
RC	RNA 105.		
RC	MEIDLINE:97089656;	PubMed:8964497;	Ghosh B.K.;
RC	"the complete nucleotide sequence of the Bacillus licheniformis S-layer encoding gene."		Malathy P.
RL	Gene 17:189-194 (1996).		
CC	-1- FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA.		
CC	-1- SUBCELLULAR LOCATION: Cell wall.		
CC	-1- SIMILARITY: CONTAINS 3 S-LAYER HOMOLOGY (SLH) DOMAINS.		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.ebi.ac.uk/announce.html">http://www.ebi.ac.uk/announce.html</a> or send an email to license@ebi.ac.uk).		
EMBL: USBB042; ANC4405; 1 ..			
DR	Infernal: IPRO0119; SLR.		
DR	Protein: P00399; Subj.: S-layer: Repeating unit.		
KW	Ceiling; Cell wall; S-layer; SIGNAL; Wall.		
FT	Peptide signal sequence	1 .. 30	POTENTIAL
FT	CHIRIN	31 .. 814	S-LAYER PROTEIN.
FT	DORAN	33 .. 155	SLH 1.
FT	DOUGLASS	98 .. 217	SLH 1.
FT	DOUGLASS	156 .. 307	SLH 1.
FT	SEEDINGS	874 AA.	SL224 MH: EEDICA4F27D2AF CRC64;
Qy	Query Match Similarity	6.81;	Score: 87;
Qy	Best Local Similarity	22.88;	DB: 1;
Matches	Conservative	28;	Length: 874;
Qy	Matches	28;	Pred. No. 8.8;
Qy	28	28	Indels 96; Gaps 14
Qy	6	6	WYKKTULKFI 48
Qy	6	6	WYLDGVNHHFPSVSEGEGDQT-----WYKKTULKFI 48
Qy	551	551	KVPPVONGKVVKDVTNTNGSGSSKKVYKNGVATGTFHNPNASGSGSYHUVVFT 610
Db	49	49	CITPEKLPVMPFLV-----MPLSGLQCEPSVPHAKQDFPKSAMHESYQYR 97
Qy	611	611	KNTGCHAPRLDLSKAGKGRADTA-----LGAFTVAYOQSHNTTCGAVADADLASY--EF 668
Db	98	98	TFFPKDGKTYKRAVEKFQDPVNLTELKGID--*PKENGLGHKLEYNKNYHNYIM 154
Qy	669	669	RV-----GNDKTS-SAKIEGKTLKVTGKTAGH-ATIVTQENIQIT 721
Db	155	155	ADKQR-----NGIKVNFKIRHN--IEDSYQLADH 162
Qy	722	722	SYRKPVDEVEQEPIRKVNIDRVYKVSDDYDGLTKLISHEKVRIVDCTEQO--- 777
Qy	183	183	YQONTPFGDGPFLPDNHYLSTQSALSQPKNEKRDNHVLGIFTVA 227
Db	778	778	--GKV-----YLDNDNAFDQND----VALGVYTA 802

RESULT 5

DN 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Cytochrome P450 51 (EC 1.14.14.-) (CYP1) (P450-L1A1) (Sterol 14-  
 alpha-demethylase) (Lanosterol 14-alpha demethylase) (P450-14DM).  
 DE ERG11 or CYP51.  
 GS Candida glabrata (Yeast) ('Torulopsis glabrata').  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 Saccharomyctales; mitosporic Saccharomyctales; Candida.  
 ID D152\_HAEIN  
 RN 11  
 RN NCBI\_TOXID=5478;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=2001-15;  
 RX MEDLINE=9616126; PubMed=8593007;  
 RA Geber A., Hitchcock C.A., Szwarc J.E., Pullen F.S., Maraden K.E.,  
 Kwon-Chung K.J., Bennett J.E.; *Deletion of the Candida glabrata erg3 and erg11 genes: effect on cell*  
 RT visibility, cell growth, sterol composition, and antifungal  
 RT susceptibility.

RT Antimicrob Agents Chemother. 39:2708-2717(1995).

RN 12

RP SEQUENCE OF 60-473 FROM N.A.

RC STRAIN=ATCC 2001;

RX MEDLINE=95081364; PubMed=7989540;

RA Bureiner-Kairuz P., Zuber J.P., Jaunin P., Buchman T.G., Bille J.,  
 Rossier M.;

RT "Rapid detection and identification of *Candida albicans* and  
*Torulopsis* (*Candida*) *glabrata* in clinical specimens by a  
 species-specific nested PCR amplification of a cytochrome P-450

RT fragment." *J Clin Microbiol*. 32:1802-1807(1994).

RL J. Clin. Microbiol. 32:1802-1807(1994).

CC -1 FUNCTIONAL CATALYSIS C14 DEMETHYLATION OF LANOSTEROL WHICH IS  
 CRITICAL FOR ERGOSTEROL BIOSYNTHESIS. IT TRANSFORMS LANOSTEROL  
 INTO 4,4'-DIMETHYL CHOLEST-8,14,24-TRIEN-3-BETA-OL.

CC -1 (BY SIMILARITY).

CC -1 PATHWAY: Ergosterol biosynthesis.

CC -1 SIMILARITY. BELONGS TO THE CYTOCHROME P450 FAMILY.

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 or send an email to license@isb-sib.ch).

DR EMBL: L40389; AAC02229; 1; -

DR INBMB: ST5389; AAC02279; 1; -

DR Pfam: PF00057; P50; 1.

DR PRINTS: PR00385; P40.

DR PROSITE: PS00006; Cytochrome P450; 1.

KW Electron transport; Oxidoreductase; Membrane; Heme;

KW Sterol biosynthesis.

FT BINDING 472 472 HME (BY SIMILARITY).  
 FT CONF1C 64 64 I -> M (IN REF 2).  
 FT CONF1C 473 473 I -> T (IN REF 2).  
 SQ SEQUENCE 533 AA: 61305 MR: A0506C17507865EP7 CRO64;

Query Match 6.8%; Score 86.5; DB: 1; Length: 533;  
 Best Local Similarity 21.4%; Pred. No. 5.3; Mismatches 81; Indels 49; Gaps 8;

Matches 44; Conservative 32; Mismatches 81; Indels 49; Gaps 8;

DR 25 GHPSVSY--DESEGDDATGKTFIKLIFCITGGLAEVPPKPVPLTVLSYGVOCFSXRDH--M 79

DR 109 GHFFTFNKLADYASAYAISHL--TTPVPGTYCDNCNMHL 149

DR 100 FPKDQNDYTAKEVYKPEGDLNRPTEKGKDFD 148

DR 487 FPFYDQNSDTSNTYNTKTYCSNTYL-GPVVNENNNTYCLGHTYNTISNFALLEN-- 542

DR 149 HNTYNAIQK-OKNIKNTFIRHNEDGSVLAQDHYQQ-- 196

DR 543 RNLZLQMFMRKNSKIN-- 593

DR 197 P-TNNHLYSTOSASKDPNEKRDHMLVLLGTVTAGITLG 233

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GS Candida glabrata (Yeast) ('Torulopsis glabrata').

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

Saccharomyctales; mitosporic Saccharomyctales; Candida.

ID D152\_HAEIN  
 RN 11  
 RN NCBI\_TOXID=5478;

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DR PROSITE: PS00006; Cytochrome P450; 1.

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 FT CONF1C 64 64 I -> M (IN REF 2).  
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RC STRAIN=2001-15;

RX MEDLINE=9616126; PubMed=8593007;

RA Geber A., Hitchcock C.A., Szwarc J.E., Pullen F.S., Maraden K.E.,  
 Kwon-Chung K.J., Bennett J.E.; *Deletion of the Candida glabrata erg3 and erg11 genes: effect on cell*  
 RT visibility, cell growth, sterol composition, and antifungal  
 RT susceptibility.

RT Antimicrob Agents Chemother. 39:2708-2717(1995).

RN 12

RP SEQUENCE OF 60-473 FROM N.A.

RC STRAIN=ATCC 2001;

RX MEDLINE=95081364; PubMed=7989540;

RA Bureiner-Kairuz P., Zuber J.P., Jaunin P., Buchman T.G., Bille J.,  
 Rossier M.;

RT "Rapid detection and identification of *Candida albicans* and  
*Torulopsis* (*Candida*) *glabrata* in clinical specimens by a  
 species-specific nested PCR amplification of a cytochrome P-450

RT fragment." *J Clin Microbiol*. 32:1802-1807(1994).

RL J. Clin. Microbiol. 32:1802-1807(1994).

CC -1 FUNCTIONAL CATALYSIS C14 DEMETHYLATION OF LANOSTEROL WHICH IS  
 CRITICAL FOR ERGOSTEROL BIOSYNTHESIS. IT TRANSFORMS LANOSTEROL  
 INTO 4,4'-DIMETHYL CHOLEST-8,14,24-TRIEN-3-BETA-OL.

CC -1 (BY SIMILARITY).

CC -1 PATHWAY: Ergosterol biosynthesis.

CC -1 SIMILARITY. BELONGS TO THE CYTOCHROME P



DPOL_HPBHE	DPOL_HPBHE	STANDARD;	PRT;	788 AA.
ID	DPOL_HPBHE			
ID	P13867			
AC	Q1-JAN-1990 (Rel.: 13; Last sequence update)			
DT	01-JAN-1990 (Rel.: 13; Last sequence update)			
DT	16-OCT-2001 (Rel.: 40; Last annotation update)			
DE	Includes: DNA-directed DNA Polymerase (EC 2.7.7.7); RNA-directed DNA Polymerase (EC 2.7.7.49); Ribonuclease II (EC 3.1.26.4).			
DP				
GN				
OS	Heron hepatitis b virus.			
OS	Viruses; Retroviridae; Hepadnaviridae; Avihepadnavirus.			
OX	[1]			
OX	NCBI_TaxID:28300;			
RN				
RP	SEQUENCE FROM N_A.			
RX	PubMed:8833160;			
RX	Medline:8833160;			
RA	Sprenger R., Kaler B. P., Will H.;			
RA	'Isolation and characterization of a hepatitis B virus endemic in hexons.'			
RT	J. Virol. 62:3832-3839(1988).			
RT	-1 - CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphated [DNA] (N).			
CC	-1 - CATALYTIC ACTIVITY: Endonucleaseolytic cleavage to 5'-			
CC	CC phosphomonoester.			
CC				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <a href="http://www.isb.ch/announce">http://www.isb.ch/announce</a> or send an email to license@isb.ch).			
CC				
CC	EMBL: M2056; AAAA5781; -.			
CC	DR PIR: A30082; J0YV1H;			
CC	DR InterPro: IPR00162; DNAPOL_viral_C.			
CC	DR InterPro: IPR00201; DNAPOL_viral_N.			
CC	DR InterPro: IPR00217; DNAPSE.			
CC	PFAM: PF00078; tvt_1.			
CC	PFAM: PF00242; DNA_pol_viral_N_1.			
CC	PFAM: PF00336; DNAPOL_viral_C_1.			
CC	Transferring; Nucleic acid-directed DNA Polymerase; DNA-directed DNA Polymerase; Nucleic acid endonuclease; DNA replication; DNA-binding.			
CC	SEQUENCE 788 AA;			
CC	90070 MW;			
CC				
DR	Query Match Similarity 19.7%; Score 85.5; DB 1; Length 788;			
DR	Best Local Similarity 19.7%; Score 85.5; DB 1; Length 788;			
DR	Matches 40; Conservative 32; Mismatches 66; Indels 65; Gaps			
DR				
DR	58 WPTLVTTLSGVQCPSSPKPHAKH---DFKFRAMPFGYVOERT---IIFPFDGNGK			
DR	139 WPKSLKSLPYPHSQVKPKYPPQDNNEELVNDYLNLPEAQLIKVSKHLVTK---GPFP			
DR				
DR	109 T-----RAYEVGSDFLVNRLLKGDFKDQNLGHKLKEVNTSYVIT			
DR	197 TWEQRHIVPOQGAYSSKINDQSRRRRTATSRNDSPI-----FRAH-----			
DR				
DR	155 ADKRGKNGVNPFLKRLDGGVQDADHYO-----QTPPIGGPVLL-PDNNH			
DR	246 -----NSGRKIST---HSTRGDSRHSUQSRTDTSFAGLAGGDSPTIGGSTAAHSPTHV			
DR				
DR	203 STQ-----SALSKDPMER 216			
DR	298 DERRRQGQVQLQASRPEST 320			
DR				
DR	RESULT 11			
DR	D153_HAELIN			
DR	D153_HAELIN STANDARD;			
DR	AC 036259;			
DR	DT 16-OCT-2001 (Rel.: 40; Created)			
DR	DT 16-OCT-2001 (Rel.: 40; Last sequence update)			
DR	DT 16-OCT-2001 (Rel.: 40; Last annotation update)			

**RC TISSUE-LIVER;**  
**RX MEDINE#7420688; Published#9276673;**  
**RX Nakanishi T., Suzuki Y., Yamamoto T., Sinohara H.;**  
**RT Molecular cloning and sequencing of cDNAs encoding three heavy-chain**  
**RT precursors of the inter-alpha-trypsin inhibitor in Syrian hamster:**  
**RT implications for the evolution of the inter-alpha-trypsin inhibitor**  
**RT heavy chain family.\*;**  
**J. Biochem. 122:71-82(1997).**

**RL RN**  
**RP SEQUENCE OF 31-50; 446-472 AND 504-523, AND SUBUNITS.**  
**RC TISSUE-Plasma;**  
**RX MEDINE#7418341; Published#8864857;**  
**RX MEDINE#7418341; Published#8864857;**  
**RX**  

**RX Yamamoto T., Yamamoto K., Sinohara H.;**  
**RT "Inter-alpha-trypsin inhibitor and its related proteins in Syrian**  
**RT hamster urine and plasma."**  
**J. Biochem. 120:141-152(1996).**

**CC -1 FUNCTION: MAY ACT AS A CARRIER OF HYALURONAN IN SERUM OR AS A**  
**CC BINDING PROTEIN BETWEEN HYALURONAN AND OTHER MATRIX PROTEIN,**  
**CC INCLUDING THOSE ON CELL SURFACES IN TISSUES TO REGULATE THE**  
**CC LOCALIZATION, SYNTHESIS AND DEGRADATION OF HYALURONAN WHICH ARE**  
**CC ESSENTIAL TO CELLS UNDERGOING BIOLOGICAL PROCESSES (IV**  
**CC SIMILARITY).**

**CC -1 PLASMA PROTEASE INHIBITORS ARE ASSEMBLED FROM**  
**CC ONE OR TWO HEAVY CHAINS (H1, H2 OR H3) AND ONE LIGHT CHAIN,**  
**CC BIKUNIN, INTER-ALPHA-INHIBITOR (I-ALPHA-I) IS COMPOSED OF H1, H2**  
**CC AND BIKUNIN, INTER-ALPHA-LIKE INHIBITOR (I-ALPHA-LII) OF H2 AND**  
**CC BIKUNIN, AND PRE-ALPHA-INHIBITOR (P-ALPHA-I) OF H3 AND BIKUNIN.**

**CC -1 PM: HEAVY CHAINS ARE INTERLINKED WITH BIKUNIN VIA A CHONDROITIN**  
**CC 4-SULFATE BRIDGE TO THE THEIR C-TERMINAL ASPARTATE (IX**  
**CC SIMILARITY).**

**CC -1 SIMILARITY: BELONGS TO THE ITIH FAMILY.**

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DR	EMBL; DR9287; PDB1940; 1..	POTENTIAL.
INTERPRO	IPR021391; VWF-A..	BY SIMILARITY.
PFAM	PF00092; VWA..	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H3..
SMART	SM00327; VWA..	BY SIMILARITY.
DR PROSTINE	P50324; VWA..	N LINKED (GLCNAC.. .) (POTENTIAL).
KW	Glycoprotein.	N LINKED (GLCNAC.. .) (POTENTIAL).
KW	Glycoprotein.	CHONDROITIN 4-SULFATE, CROSS-LINK SITE
SIGNAL	1	18
PT	PROPEP	POTENTIAL.
FT	PROPEP	19
FT	CHAIN	31
FT	PROPEP	647
FT	DONAI	279
FT	CARBHDY	98
FT	CARBHDY	577
FT	BINDING	646

[1] SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 MEDLINE-# 91273991; Pubmed-# 204189;  
 Wendland B.; Miller K.G.; Schilling J.; Scheller R.H.;  
 "Differentiation expression of the P56 gene family";  
 Neuron 6:993-1007(1991).  
 -I- FUNCTION: MAY HAVE A REGULATORY ROLE IN THE MEMBRANE INTERACTIONS  
 DURING TRAFFICKING OF SYNAPTIC VESICLES AT THE ACTIVE ZONE OF THE  
 SYNAPSE. IT FINDS ACIDIC PHOSPHOLIPIDS WITH A SPECIFICITY THAT  
 REQUIRES THE PRESENCE OF BOTH AN ACIDIC HEAD GROUP AND A DIACYL  
 BACKBONE.  
 -I- SUBUNIT: HOMODIMER OR HOMOHETRIMER (POSSIBLE).  
 -I- SUBCELLULAR LOCATION: SYNAPTIC VESICLES IN NEURONS.  
 -I- TISSUE SPECIFICITY: SPINAL CORD, BRAINSTEM, MIDBRAIN, AND ELECTRIC  
 ORGAN.  
 -I- SIMILARITY: CONTAINS 2 C2 DOMAINS.  
 -I- SIMILARITY: BELONGS TO THE SYNATOGAMIN FAMILY.

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 entities requires a license agreement (See <http://www.ebi.ac.uk/swissprot/announcements.html>).

EMBL: M61276; AM49228; 1.; -		
PIR: JH0144;		
PIRSP: JH0144;		
HSPO: 321701; JBN		
Inter-PO: IPR000008;	C2	
Inter-PRO: IPR002195;	Uni	
Inter-PRO: IPR001155;	Uni	
Inter-Pro: IPR001666;	C2	
Inter-Pro: IPR003666;	C2	
PRINTS: PR0339; C2-1;	2- DOMAIN	
SMART: SM04039; C2-2;		
PROSITE: PS00449; C2-DOMAIN; 1;		
PROSITE: PS00004; C2-DOMAIN; 2;		
KW	Multigene family; Glycoprotein.	
DOMAIN	1	VESICULAR (POTENTIAL).
TRANSMEMBRANE	74	
DOMAIN	75	POTENTIAL.
TRANSMEMBRANE	101	CYTOSLASMIC (POTENTIAL).
DOMAIN	102	
TRANSMEMBRANE	439	
DOMAIN	153	PHOSPHOLIPID BINDING (PROBABLE).
TRANSMEMBRANE	399	
DOMAIN	173	C2 DOMAIN 1.
TRANSMEMBRANE	262	C2 DOMAIN 2.
CARBOHYDRT	304	
CARBOHYDRT	6	N-LINKED (GLCNAC. . .) (POTENTIAL).
CARBOHYDRT	6	N-LINKED (GLCNAC. . .) (POTENTIAL).
SEQUENCE	46	N-LINKED (GLCNAc6F39 CRCG4; . . .) (POTENTIAL).
SEQUENCE	49 AA;	49278 MB;
SEQUENCE	50	20133F6C65F39 CRCG4;

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Matches 44; Conservative 40; Mismatches 75; Indels 29; Gaps 9;

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Qy 65 LSYGQCPSPYDPDHMKQHDFPKSAMPEGVQERTIFPKDDGNYTRAEVKPGDLYNRI 124  
1 MSKEIKKYSVDPKEYRPLDYLLECKTIDQF -- DQFLERSKKLKIR -DSKYQNL 56

Db 125 E--LKGIDFEDDNFLGHKPLEYYNSHNVYI -MADKONGIKWNEKTRH--- NIEDSS 176

Qy 57 ESKYLESLKLFEDNLLANKKI -IN YISNLISYNDVSHFREISOKEMFMYSEFNQIDEN 115

Db 177 VOLADHQQTNPPIGDGPVLIP --- DNHYLSTQSALSKDNEKRDHMVLGFTRAAGIT 231

Qy 116 QRILHEBKTKWLDPLASYYKALDFVERSKRHLASK -- EWEYLI------ KVS 164

Db 232 LOMDELYK 239

Qy 165 RGNTELYK 172

Search completed: June 3, 2003, 15:07:06  
Job time : 24 secs